

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/553,520
Source: PUT
Date Processed by STIC: 10/28/05

ENTERED



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/553,520

DATE: 10/28/2005

TIME: 09:36:54

Input Set : A:\33178SEQLIST.TXT

Output Set: N:\CRF4\10282005\J553520.raw

```

4 <110> APPLICANT: Bodian, Dale
5      Daouti, Sherif
6      Kumar, Chandrika
7      Latario, Brian
8      Quintavalla, Joseph
11 <120> TITLE OF INVENTION: High throughput functional genomic
12      screening methods for osteoarthritis
15 <130> FILE REFERENCE: 4-33178
C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/553,520
C--> 17 <141> CURRENT FILING DATE: 2005-10-14
17 <150> PRIOR APPLICATION NUMBER: 60/463,933
18 <151> PRIOR FILING DATE: 2003-04-18
20 <160> NUMBER OF SEQ ID NOS: 180
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 21
26 <212> TYPE: DNA
27 <213> ORGANISM: unknown
29 <220> FEATURE:
30 <223> OTHER INFORMATION: primer sequence which can bind to any organism
32 <400> SEQUENCE: 1
33 tttccctggc aaggactatg a                                21
35 <210> SEQ ID NO: 2
36 <211> LENGTH: 17
37 <212> TYPE: DNA
38 <213> ORGANISM: unknown
40 <220> FEATURE:
41 <223> OTHER INFORMATION: primer sequence which can bind to any organism
43 <400> SEQUENCE: 2
44 aatggcggtga gtcgggc                                    17
46 <210> SEQ ID NO: 3
47 <211> LENGTH: 26
48 <212> TYPE: DNA
49 <213> ORGANISM: unknown
51 <220> FEATURE:
52 <223> OTHER INFORMATION: primer sequence which can bind to any organism
54 <400> SEQUENCE: 3
55 tgatctcttt tggaattaag gagcat                            26
57 <210> SEQ ID NO: 4
58 <211> LENGTH: 23
59 <212> TYPE: DNA
60 <213> ORGANISM: unknown
62 <220> FEATURE:

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63 <223> OTHER INFORMATION: primer sequence which can bind to any organism
65 <400> SEQUENCE: 4
66 atgggcatct cctccataat ttg                                     23
68 <210> SEQ ID NO: 5
69 <211> LENGTH: 19
70 <212> TYPE: DNA
71 <213> ORGANISM: unknown
73 <220> FEATURE:
74 <223> OTHER INFORMATION: primer sequence which can bind to any organism
76 <400> SEQUENCE: 5
77 aaattgctgg cagggttgc                                         19
79 <210> SEQ ID NO: 6
80 <211> LENGTH: 21
81 <212> TYPE: DNA
82 <213> ORGANISM: unknown
84 <220> FEATURE:
85 <223> OTHER INFORMATION: primer sequence which can bind to any organism
87 <400> SEQUENCE: 6
88 tttctgtact gcgggtggaa c                                       21
90 <210> SEQ ID NO: 7
91 <211> LENGTH: 19
92 <212> TYPE: DNA
93 <213> ORGANISM: unknown
95 <220> FEATURE:
96 <223> OTHER INFORMATION: primer sequence which can bind to any organism
98 <400> SEQUENCE: 7
99 gcaaacccttc aaggcagcc                                         19
101 <210> SEQ ID NO: 8
102 <211> LENGTH: 19
103 <212> TYPE: DNA
104 <213> ORGANISM: unknown
106 <220> FEATURE:
107 <223> OTHER INFORMATION: primer sequence which can bind to any organism
109 <400> SEQUENCE: 8
110 tgctgtttgc ctccgacat                                         19
112 <210> SEQ ID NO: 9
113 <211> LENGTH: 16
114 <212> TYPE: DNA
115 <213> ORGANISM: unknown
117 <220> FEATURE:
118 <223> OTHER INFORMATION: primer sequence which can bind to any organism
120 <400> SEQUENCE: 9
121 acgctgctcg tcgccg                                           16
123 <210> SEQ ID NO: 10
124 <211> LENGTH: 20
125 <212> TYPE: DNA
126 <213> ORGANISM: unknown
128 <220> FEATURE:
129 <223> OTHER INFORMATION: primer sequence which can bind to any organism

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131 <400> SEQUENCE: 10
132 gccagcctcc tggacatcct                                20
134 <210> SEQ ID NO: 11
135 <211> LENGTH: 23
136 <212> TYPE: DNA
137 <213> ORGANISM: unknown
139 <220> FEATURE:
140 <223> OTHER INFORMATION: primer sequence which can bind to any organism
142 <400> SEQUENCE: 11
143 acccaacacc aagacacagt tct                                23
145 <210> SEQ ID NO: 12
146 <211> LENGTH: 33
147 <212> TYPE: DNA
148 <213> ORGANISM: unknown
150 <220> FEATURE:
151 <223> OTHER INFORMATION: primer sequence which can bind to any organism
153 <400> SEQUENCE: 12
154 tcttactgct atacctttac tctttatggt gta                    33
156 <210> SEQ ID NO: 13
157 <211> LENGTH: 19
158 <212> TYPE: DNA
159 <213> ORGANISM: unknown
161 <220> FEATURE:
162 <223> OTHER INFORMATION: primer sequence which can bind to any organism
164 <400> SEQUENCE: 13
165 cagccgcttc acctacagc                                    19
167 <210> SEQ ID NO: 14
168 <211> LENGTH: 25
169 <212> TYPE: DNA
170 <213> ORGANISM: unknown
172 <220> FEATURE:
173 <223> OTHER INFORMATION: primer sequence which can bind to any organism
175 <400> SEQUENCE: 14
176 ttttgtattc aatcactgtc ttgcc                                25
178 <210> SEQ ID NO: 15
179 <211> LENGTH: 20
180 <212> TYPE: DNA
181 <213> ORGANISM: unknown
183 <220> FEATURE:
184 <223> OTHER INFORMATION: primer sequence which can bind to any organism
186 <400> SEQUENCE: 15
187 gccagcctcc tggacatcct                                20
189 <210> SEQ ID NO: 16
190 <211> LENGTH: 23
191 <212> TYPE: DNA
192 <213> ORGANISM: unknown
194 <220> FEATURE:
195 <223> OTHER INFORMATION: primer sequence which can bind to any organism
197 <400> SEQUENCE: 16

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198 agtcctttca ggctagctgc atc 23
200 <210> SEQ ID NO: 17
201 <211> LENGTH: 17
202 <212> TYPE: DNA
203 <213> ORGANISM: unknown
205 <220> FEATURE:
206 <223> OTHER INFORMATION: primer sequence which can bind to any organism
208 <400> SEQUENCE: 17
209 tcgaggacag cgaggcc 17
211 <210> SEQ ID NO: 18
212 <211> LENGTH: 22
213 <212> TYPE: DNA
214 <213> ORGANISM: unknown
216 <220> FEATURE:
217 <223> OTHER INFORMATION: primer sequence which can bind to any organism
219 <400> SEQUENCE: 18
220 tcgaggggtgt agcgtgtaga ga 22
222 <210> SEQ ID NO: 19
223 <211> LENGTH: 19
224 <212> TYPE: DNA
225 <213> ORGANISM: unknown
227 <220> FEATURE:
228 <223> OTHER INFORMATION: primer sequence which can bind to any organism
230 <400> SEQUENCE: 19
231 atggggaagg tgaaggctcg 19
233 <210> SEQ ID NO: 20
234 <211> LENGTH: 20
235 <212> TYPE: DNA
236 <213> ORGANISM: unknown
238 <220> FEATURE:
239 <223> OTHER INFORMATION: primer sequence which can bind to any organism
241 <400> SEQUENCE: 20
242 taaaagcagc cctggtgacc 20
244 <210> SEQ ID NO: 21
245 <211> LENGTH: 19
246 <212> TYPE: DNA
247 <213> ORGANISM: unknown
249 <220> FEATURE:
250 <223> OTHER INFORMATION: primer sequence which can bind to any organism
252 <400> SEQUENCE: 21
253 caagtttgta caaaaaagc 19
255 <210> SEQ ID NO: 22
256 <211> LENGTH: 19
257 <212> TYPE: DNA
258 <213> ORGANISM: unknown
260 <220> FEATURE:
261 <223> OTHER INFORMATION: primer sequence which can bind to any organism
263 <400> SEQUENCE: 22
264 accactttgt acaagaaag 19

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```

266 <210> SEQ ID NO: 23
267 <211> LENGTH: 836
268 <212> TYPE: PRT
269 <213> ORGANISM: homo sapiens
271 <400> SEQUENCE: 23
272 Met Ile Pro Phe Leu Pro Met Phe Ser Leu Leu Leu Leu Leu Ile Val
273   1           5           10           15
274 Asn Pro Ile Asn Ala Asn Asn His Tyr Asp Lys Ile Leu Ala His Ser
275           20           25           30
276 Arg Ile Arg Gly Arg Asp Gln Gly Pro Asn Val Cys Ala Leu Gln Gln
277           35           40           45
278 Ile Leu Gly Thr Lys Lys Lys Tyr Phe Ser Thr Cys Lys Asn Trp Tyr
279           50           55           60
280 Lys Lys Ser Ile Cys Gly Gln Lys Thr Thr Val Leu Tyr Glu Cys Cys
281 65           70           75           80
282 Pro Gly Tyr Met Arg Met Glu Gly Met Lys Gly Cys Pro Ala Val Leu
283           85           90           95
284 Pro Ile Asp His Val Tyr Gly Thr Leu Gly Ile Val Gly Ala Thr Thr
285           100          105          110
286 Thr Gln Arg Tyr Ser Asp Ala Ser Lys Leu Arg Glu Glu Ile Glu Gly
287           115          120          125
288 Lys Gly Ser Phe Thr Tyr Phe Ala Pro Ser Asn Glu Ala Trp Asp Asn
289           130          135          140
290 Leu Asp Ser Asp Ile Arg Arg Gly Leu Glu Ser Asn Val Asn Val Glu
291 145          150          155          160
292 Leu Leu Asn Ala Leu His Ser His Met Ile Asn Lys Arg Met Leu Thr
293           165          170          175
294 Lys Asp Leu Lys Asn Gly Met Ile Ile Pro Ser Met Tyr Asn Asn Leu
295           180          185          190
296 Gly Leu Phe Ile Asn His Tyr Pro Asn Gly Val Val Thr Val Asn Cys
297           195          200          205
298 Ala Arg Ile Ile His Gly Asn Gln Ile Ala Thr Asn Gly Val Val His
299           210          215          220
300 Val Ile Asp Arg Val Leu Thr Gln Ile Gly Thr Ser Ile Gln Asp Phe
301 225          230          235          240
302 Ile Glu Ala Glu Asp Leu Ser Ser Phe Arg Ala Ala Ala Ile Thr
303           245          250          255
304 Ser Asp Ile Leu Glu Ala Leu Gly Arg Asp Gly His Phe Thr Leu Phe
305           260          265          270
306 Ala Pro Thr Asn Glu Ala Phe Glu Lys Leu Pro Arg Gly Val Leu Glu
307           275          280          285
308 Arg Phe Met Gly Asp Lys Val Ala Ser Glu Ala Leu Met Lys Tyr His
309           290          295          300
310 Ile Leu Asn Thr Leu Gln Cys Ser Glu Ser Ile Met Gly Gly Ala Val
311 305          310          315          320
312 Phe Glu Thr Leu Glu Gly Asn Thr Ile Glu Ile Gly Cys Asp Gly Asp
313           325          330          335
314 Ser Ile Thr Val Asn Gly Ile Lys Met Val Asn Lys Lys Asp Ile Val
315           340          345          350

```

VERIFICATION SUMMARY

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L:17 M:270 C: Current Application Number differs, Replaced Current Application No
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:8290 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (163) SEQUENCE:
L:8295 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (164) SEQUENCE:
L:8300 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (165) SEQUENCE:
L:8305 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (166) SEQUENCE: